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RAW SEQUENCE LISTING

DATE: 07/19/2002

PATENT APPLICATION: US/09/985,689A

TIME: 15:11:39

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3 <110> APPLICANT: HATADA, YUJI
 4 OGAWA, AKINORI
 5 KAGEYAMA, YASUSHI
 6 SATO, TSUYOSHI
 7 ARAKI, HIROYUKI
 8 SUMITOMO, NOBUYUKI
 9 OKUDA, MITSUYOSHI
 10 SAEKI, KATSUHIISA
 12 <120> TITLE OF INVENTION: Alkaline proteases
 14 <130> FILE REFERENCE: 215483US0
 16 <140> CURRENT APPLICATION NUMBER: US 09/985,689A
 C--> 17 <141> CURRENT FILING DATE: 2002-07-01
 19 <150> PRIOR APPLICATION NUMBER: JP P2000-355166
 20 <151> PRIOR FILING DATE: 2000-11-22
 22 <150> PRIOR APPLICATION NUMBER: JP P2001-114048
 23 <151> PRIOR FILING DATE: 2001-04-12
 25 <160> NUMBER OF SEQ ID NOS: 7
 27 <170> SOFTWARE: PatentIn version 3.1
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 32 <213> ORGANISM: Bacillus sp.
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 37 1 5 10 15
 40 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
 41 20 25 30
 44 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
 45 35 40 45
 48 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
 49 50 55 60
 52 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
 53 65 70 75 80
 56 Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
 57 85 90 95
 60 Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
 61 100 105 110
 64 Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
 65 115 120 125
 68 Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
 69 130 135 140
 72 Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
 73 145 150 155 160

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77           165           170           175
80 Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
81           180           185           190
84 Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
85           195           200           205
88 Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
89           210           215           220
92 Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
93 225           230           235           240
96 Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
97           245           250           255
100 Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
101           260           265           270
104 Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
105           275           280           285
108 Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
109           290           295           300
112 Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
113 305           310           315           320
116 Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
117           325           330           335
120 Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
121           340           345           350
124 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
125           355           360           365
128 Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
129           370           375           380
132 Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu
133 385           390           395           400
136 Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
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150 <212> TYPE: PRT
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160           20           25           30
163 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
164           35           40           45
167 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
168           50           55           60
171 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly

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180          100          105          110
183 Thr Leu Phe Ser Gln Ala Phe Ser Ala Gly Ala Arg Ile His Thr Asn
184          115          120          125
187 Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
188          130          135          140
191 Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
192 145          150          155          160
195 Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
196          165          170          175
199 Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
200          180          185          190
203 Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg
204          195          200          205
207 Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
208          210          215          220
211 Thr Tyr Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
212 225          230          235          240
215 Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
216          245          250          255
219 Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
220          260          265          270
223 Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
224          275          280          285
227 Leu Ile Ala Gly Ala Ala Asp Val Gly Leu Gly Tyr Pro Asn Gly Asn
228          290          295          300
231 Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
232 305          310          315          320
235 Val Asn Glu Ser Ser Ala Leu Ser Thr Ser Gln Lys Ala Thr Tyr Thr
236          325          330          335
239 Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
240          340          345          350
243 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
244          355          360          365
247 Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Arg Tyr Val Gly Asn Asp
248          370          375          380
251 Phe Ser Ala Pro Phe Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu
252 385          390          395          400
255 Asn Val Phe Ile Asn Ser Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
256          405          410          415
259 Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Asn Phe Ser Leu Ala Ile
260          420          425          430
263 Val Asn
267 <210> SEQ ID NO: 3
268 <211> LENGTH: 433
269 <212> TYPE: PRT

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270 <213> ORGANISM: Bacillus sp.
272 <400> SEQUENCE: 3
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278 Tyr Gly Leu Tyr Gly Gln Gly Gln Val Val Ala Val Ala Asp Thr Gly
279          20          25          30
282 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
283          35          40          45
286 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
287          50          55          60
290 Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
291 65          70          75          80
294 Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
295          85          90          95
298 Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
299          100         105         110
302 Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
303          115         120         125
306 Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
307          130         135         140
310 Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
311 145         150         155         160
314 Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
315          165         170         175
318 Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
319          180         185         190
322 Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
323          195         200         205
326 Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
327          210         215         220
330 Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
331 225         230         235         240
334 Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
335          245         250         255
338 Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
339          260         265         270
342 Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
343          275         280         285
346 Ile Ala Gly Ala Thr Asp Val Gly Leu Gly Tyr Pro Ser Gly Asp Gln
347          290         295         300
350 Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr Val
351 305         310         315         320
354 Asn Glu Ala Thr Ala Leu Thr Thr Gly Gln Lys Ala Thr Tyr Ser Phe
355          325         330         335
358 Gln Thr Gln Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Thr Asp
359          340         345         350
362 Ala Pro Gly Ser Thr Thr Ala Ser Tyr Thr Leu Val Asn Asp Leu Asp
363          355         360         365
366 Leu Val Ile Thr Ala Pro Asn Gly Gln Lys Tyr Val Gly Asn Asp Phe

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367      370      375      380
370 Ser Tyr Pro Tyr Asp Asn Asn Trp Asp Gly Arg Asn Asn Val Glu Asn
371 385      390      395      400
374 Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val Gln
375      405      410      415
378 Ala Tyr Asn Val Pro Ser Gly Pro Gln Arg Phe Ser Leu Ala Ile Val
379      420      425      430
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387 <211> LENGTH: 433
388 <212> TYPE: PRT
389 <213> ORGANISM: Bacillus sp.
391 <400> SEQUENCE: 4
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398      20      25      30
401 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
402      35      40      45
405 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Ser Asp
406      50      55      60
409 Pro Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Ala
410 65      70      75      80
413 Leu Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser Ile
414      85      90      95
417 Met Asp Ser Ser Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Asn Thr
418      100     105     110
421 Leu Phe Ser Gln Ala Trp Asn Ala Gly Ala Arg Ile His Thr Asn Ser
422      115     120     125
425 Trp Gly Ala Pro Val Asn Gly Ala Tyr Thr Ala Asn Ser Arg Gln Val
426      130     135     140
429 Asp Glu Tyr Val Arg Asn Asn Asp Met Thr Val Leu Phe Ala Ala Gly
430 145     150     155     160
433 Asn Glu Gly Pro Asn Ser Gly Thr Ile Ser Ala Pro Gly Thr Ala Lys
434      165     170     175
437 Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Tyr Arg Pro Ser Phe Gly
438      180     185     190
441 Ser Ile Ala Asp Asn Pro Asn His Ile Ala Gln Phe Ser Ser Arg Gly
442      195     200     205
445 Ala Thr Arg Asp Gly Arg Ile Lys Pro Asp Val Thr Ala Pro Gly Thr
446      210     215     220
449 Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe Trp
450 225     230     235     240
453 Ala Asn Tyr Asn Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met Ala
454      245     250     255
457 Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe Ile
458      260     265     270
461 Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Ile Lys Ala Ala Leu
462      275     280     285

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VERIFICATION SUMMARY

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